

SPLICE FORM 1:

```

1  CGTCCTTCCT GGTCCCTGCGG GTCCAGGACT GTCCGCGGGG TTGAGGGAAG
51  GGGCCGTGCC CGGTGCCAGC CCAGGTGCTC GCGGCCTGGC TCCATGGCCC
101 TGGTCACAGT GAGCCGTTTCG CCCCCGGGCA GCGGCGCCTC CACGCCCCTG
151 GGGCCCTGGG ACCAGGCGGT CCAGCGAAGG AGTCGACTCC AGCGAAGGCA
201 GAGCTTTGCG GTGCTCCGTG GGGCTGTCCT GGGACTGCAG GATGGAGGGG
251 ACAATGATGA TGCAGCAGAG GCCAGTTCCTG AGCCAACAGA GAAGGCCCCG
301 AGTGAGGAGG AGCTCCACGG GGACCAGACA GACTTCGGGC AAGGATCCCA
351 GAGTCCCCAG AAGCAGGAGG AGCAGAGGCA GCACCTGCAC CTCATGGTAC
401 AGTCCGGGTG GCCGAGGAT GACATCCGCC TGGCAGCCCA GCTGGAGGCA
451 CCCCCGCTC CCGGCTCCG CTACCTGCTG GTAGTTTCTA CACGAGAAGG
501 AGAAGGTCTG AGCCAGGATG AGACGGTCCT CCTGGGCGTG GATTTCCCTG
551 ACAGCAGCTC CCCCAGCTGC ACCCTGGGCC TGGTCTTGCC CCTCTGGAGT
601 GACACCCAGG TGTACTTAGA TGGAGACGGG GGCTTCAGCG TGACGTCTGG
651 TGGGCAAAAGC CGGATCTTCA AGCCCATCTC CATCCAGACC ATGTGGGCCA
701 CACTCCAGGT ATTGACACAA GCATGTGAGG CAGCTCTAGG CAGCGGCCTT
751 GTACCGGGTG GCAGTGCCCT CACCTGGGCC AGCCACTACC AGGAGAGACT
801 GAACTCCGAA CAGAGCTGCC TCAATGAGTG GACGGCTATG GCCGACCTGG
851 AGTCTCTGCG GCCTCCACG GCCGAGCCTG GCGGGTCCTC AGAACAGGAG
901 CAGATGGAGC AGGCGATCCG TGCTGAGCTG TGGAAAGTGT TGGATGTCAG
951 TGACCTGGAG AGTGTCACCT CCAAAGAGAT CCGCCAGGCT CTGGAGCTGC
1001 GCCTGGGGCT CCCCCTCCAG CAGTACCGTG ACTTCATCGA CAACCAGATG
1051 CTGCTGCTGG TGGCAGACGG GGACCGAGCC TCCCGCATCT TCCCCACCT
1101 CTACCTGGGC TCAGAGTGGA ACGCAGCAAA CCTGGAGGAG CTGCAGAGGA
1151 ACAGGGTCAC CCACATCTTG AACATGGCCC GGGAGATTGA CAACTTCTAC
1201 CCTGAGCGCT TCACCTACCA CAATGTGCGC CTCTGGGATG AGGAGTCGGC
1251 CCAGCTGCTG CCGCACTGGA AGGAGACGCA CCGCTTCATT GAGGCTGCAA
1301 GAGCACAGGG CACCCACGTG CTGGTCCACT GCAAGATGGG CGTCAGCCGC
1351 TCAGCGGCCA CAGTGCTGGC CTATGCCATG AAGCAGTACG AATGCAGCCT
1401 GGAGCAGGCC CTGCGCCACG TGCAGGAGCT CCGGCCCATC GCCCGCCCA
1451 ACCCTGGCTT CCTGCGCCAG CTGCAGATCT ACCAGGGCAT CCTGACGGCC
1501 AGAACCTGAG GGTGGTGGGG AGGAGAAGGT TGTAGGCATG GAAGAGAGCC
1551 AGGCAGCCCC GAAAGAAGAG CCTGGGCCAC GGCCACGTAT AAACCTCCGA
1601 GGGGTCATGA GGTCCATCAG TCTTCTGGAG CCCTCCTTGG AGCTGGAGAG
1651 CACCTCAGAG ACCAGTGACA TGCCAGAGGT CTTCCTTCC CACGAGTCTT
1701 CACATGAAGA GCCTCTGACA CCCTTCCCAC AGCTTGCAAG GACCAAGGGA
1751 GGCCAGCAGG TGGACAGGGG GCCTCAGCCT GCCCTGAAGT CCCGCCAGTC
1801 AGTGGTTACC CTCCAGGGCA GTGCCGTGGT GGCCAACCGG ACCCAGGCCT
1851 TCCAGGAGCA GGAGCAGGGG CAGGGGCAGG GGCAGGGAGA GCCCTGCATT
1901 TCCTCTACGC CCAGGTTCOG GAAGGTGGTG AGACAGGCCA GCGTGCATGA
1951 CAGTGGAGAG GAGGGCGAGG CTTGAGCCCT CACACATGCC CACGCTCCCC
2001 TGACACTGAA GAGGATCCAC AACTCCTTGG AGAAACACCC TCACGTCTGT
2051 TGCCGCACAC ATTCTCTCA GCTCCGCCCC ATACCCGTCA CTACAGCCTC
2101 ACCTCCCACC CCTGTCACTA CGGCCTCACC TCCCACCCCT GTCACTACAG
2151 CCTCACCTCC TACAGCCTTA AGTCCCAGGC CCATGTCTGC CTGTCCAAGG
2201 GCTCAAGACT TTCTAACTGG GATGTGGTAG AGGGACTGAA GGTACCTTTG
2251 GGGGCAACAG CACCTAGTTCATTCTCAA CTCTAGCCCT GCACACTCAC
2301 CTGTGGCAGC GAATGAAAAC AGAGCTTCCC GTGCAAAAAG GGTCACGCCT
2351 CCCACCCCGG CCCCCTCCCT GCACCTCCTG TCCTCTCCA GTTCATTCTT
2401 GGAACCCAGC AGGCCAGGCA ACCAGTGGCC CCCAAAGGCA GGCAGGATCC
2451 TCAGGCCCCA GCCGCGGGAG GCTGGAAGGG CTGGCAGATC GCTTCCCTCA
2501 TCCACCTCCA CCGGTCCAGG TCTTTGCTGC TGTCCCAGA CCTCCTGTGA
2551 CACCACGCCA GATCACAGGG CACCAGGCCA GAGATAGTCT TCTTTTGTGTC
2601 CTTTCTGGCC TCTGGCTAGT CAGTTTTTCA TAGCCTTACA GTATCTGGCT
2651 TTGTACTGAG AAATAAAACA CATTTTCATA AAAAAAAAAA AAAAAAAAAA
2701 AAAA

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FEATURES:

5' UTR: 1-93
 Start: 94-1506
 Stop: 1509
 3' UTR: 1510-2704

SPLICE FORM 2:

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1 TGGTTGAGGG AAGGGGCCGT GCCCGGTGCC AGCCCAGGTG CTCGCGGCCT
51 GGCTCCATGG CCCTGGTCAC AGTGAGCCGT TCGCCCCCGG GCAGCGGCGC
101 CTCCACGCCC GTGGGGCCCT GGGACCAGGC GGTCCAGCGA AGGAGTCGAC
151 TCCAGCGAAG GCAGAGCTTT GCGGTGCTCC GTGGGGCTGT CCTGGGACTG
201 CAGGATGGAG GGGACAATGA TGATGCAGCA GAGGCCAGTT CTGAGCCAAC
251 AGAGAAGGCC CCGAGTGAGG AGGAGCTCCA CGGGGACCAG ACAGACTTCG
301 GGCAAGGATC CCAGAGTCCC CAGAAGCAGG AGGAGCAGAG GCAGCACCTG
351 CACCTCATGG TACAGCTGCT GAGGCCGAG GATGACATCC GCCTGGCAGC
401 CCAGCTGGAG GCACCCCGGC CTCCCCGGCT CCGCTACCTG CTGGTAGTTT
451 CTACACGAGA AGGAGAAGGT CTGAGCCAGG ATGAGACGGT CCTCCTGGGC
501 GTGGATTTCC CTGACAGCAG CTCCCCCAGC TGCACCCTGG GCCTGGTCTT
551 GCCCCTCTGG AGTGACACC AGGTGTACTT AGATGGAGAC GGGGGCTTCA
601 GCGTGACGTC TGGTGGGCAA AGCCGGATCT TCAAGCCCAT CTCCATCCAG
651 ACCATGTGGG CCACACTCCA GGTATTGCAC CAAGCATGTG AGGCAGCTCT
701 AGGCAGCGGC CTTGTACCGG GTGGCAGTGC CCTCACCTGG GCCAGCCACT
751 ACCAGGAGAG ACTGAAGTCC GAACAGAGCT GCCTCAATGA GTGGACGGCT
801 ATGGCCGACC TGGAGTCTCT GCGGCCCTCC AGCGCCGAGC CTGGCGGGTC
851 CTCAGAACAG GAGCAGATGG AGCAGGCGAT CCGTGCTGAG CTGTGGAAAG
901 TGTTGGATGT CAGTGACCTG GAGAGTGTCA CTTCCAAAGA GATCCGCCAG
951 GCTCTGGAGC TGCGCCTGGG GCTCCCCCTC CAGCAGTACC GTGACTTCAT
1001 CGACAACAG ATGCTGCTGC TGGTGGCACA GCGGGACCGA GCCTCCGCA
1051 TCTTCCCCCA CCTCTACTG GGCTCAGAGT GGAACGCAGC AAACCTGGAG
1101 GAGCTGCAGA GGAACAGGGT CACCCACATC TTGAACATGG CCCGGGAGAT
1151 TGACAACTTC TACCCTGAGC GCTTACCTA CCACAATGTG CGCCTCTGGG
1201 ATGAGGAGTC GGCCAGCTG CTGCCGCACT GGAAGGAGAC GCACCGCTTC
1251 ATTGAGGCTG CAAGAGCACA GGGCACCCAC GTGCTGGTCC ACTGCAAGAT
1301 GGGCGTCAGC CGCTCAGCGG CCACAGTGCT GGCCTATGCC ATGAAGCAGT
1351 ACGAATGCAG CCTGGAGCAG GCCCTGCGCC ACGTGCAGGA GCTCCGGCCC
1401 ATCGCCCGCC CCAACCCTGG CTTCTGCGC CAGCTGCAGA TCTACCAGGG
1451 CATCCTGACG GCCAGCCGCC AGAGCCATGT CTGGGAGCAG AAAGTGGGTG
1501 GGGTCTCCCC AGAGGAGCAC CCAGCCCCTG AAGTCTCTAC ACCATTCCCA
1551 CTTCTTCCGC CAGAACCTGA GGTGGTGGG GAGGAGAAGG TTGTAGGCAT
1601 GGAAGAGAGC CAGGCAGCCC CGAAAGAAGA GCCTGGGCCA CGGCCACGTA
1651 TAAACCTCCG AGGGGTCTAT AGGTCCATCA GTCTTCTGGA GCCCTCCTTG
1701 GAGCTGGAGA GCACCTCAGA GACCAGTGAC ATGCCAGAGG TCTTCTCTTC
1751 CCACGAGTCT TCACATGAAG AGCCTCTGCA GCCCTTCCCA CAGCTTGCAA
1801 GGACCAAGGG AGGCCAGCAG GTGGACAGGG GGCCTCAGCC TGCCCTGAAG
1851 TCCCGCCAGT CAGTGGTTAC CCTCCAGGGC AGTGCCGTGG TGCCAACCG
1901 GACCCAGGCC TTCCAGGAGC AGGAGCAGGG GCAGGGGCAG GGGCAGGGAG
1951 AGCCCTGCAT TTCTCTACG CCCAGGTTCC GGAAGGTGGT GAGCAGGGC
2001 AGCGTGCAAT ACAGTGGAGA GGAGGGCGAG GCCTGAGCCC TCACACATGC
2051 CCACGCTCCC CTGACACTGA AGAGGATCCA CAACTCCTTG GAGAAACACC
2101 CTCACGTCTG TTGCCGCACA CATTCCTCTC AGCTCCGCCC CATAACCGTC
2151 ACTACAGCCT CACCTCCAC CCCTGTCACT ACGGCTTAC CTCCCACCC
2201 TGTCACTACA GCCTCACCTC TTTCTAACTG GGATGTGGTA GAGGGACTGA
2251 CCTGTCCAAG GGCTCAAGAC TTTCTAACTG GGATGTGGTA GAGGGACTGA
2301 AGGTACCTTT GGGGGCAACA GCACCCTAGT TTCATTCTCA ACTCTAGCCC
2351 TGCACACTCA CCTGTGGCAC GGAATGAAAA CAGAGCTTCC CGTGCAAAAA
2401 GGGTCACGCC TCCCACCCCC GCCCCCTCCC TGCACCTCCT GTCCTCTCCC
2451 AGTTCATTC TGGAAACCAG CAGGCCAGGC AACCAGTGGC CCCCAAAGGC
2501 AGGCAGGATC CTCAGGCCCC AGCCGCGGGA GGCTGGAAGG GCTGGCAGAT
2551 CGCTTCCCTC ATCCACCTCC ACCGGTCCAG GTCTTTGTG CTGTCCCCAG
2601 ACCTCCTGTG ACACCAGGCC AGATCACAGG GCACCAGGCC AGAGATAGTC
2651 TTCTTTTTGT CCTTCTGGC CTCTGGCTAG TCAGTTTTTC ATAGCCTTAC
2701 AGTATCTGGC TTTGTACTGA GAAATAAAAC ACATTTTCAT AAAAAAAAAA
2751 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2801 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2851 AA

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FIGURE 1, page 2 of 5

FEATURES:

5' UTR: 1-56

Start: 57

Stop: 2034

3' UTR: 2037-2852

SPLICE FORM 3:

1 CCTGGTCTCTG CGGGTCCAGG ACTGTCCCGC GGGGTTGAGG GAAGGGGCCG
51 TGCCCGGTGC CAGCCCAGGT GCTCGCGGCC TGGCTCCATG GCCCTGGTCA
101 CAGTGAGCCG TTCGCCCCG GGCAGCGGCG CCTCCACGCC CGTGGGGCCC
151 TGGGACCAGG CGGTCCAGCG AAGGAGTCGA CTCCAGCGAA GGCAGAGCTT
201 TGCGGTGCTC CGTGGGGCTG TCCTGGGACT GCAGGATGGA GGGGACAATG
251 ATGATGCAGC AGAGGCCAGT TCTGAGCCAA CAGAGAAGGC CCCGAGTGAG
301 GAGGAGCTCC ACGGGGACCA GACAGACTTC GGGCAAGGAT CCCAGAGTCC
351 CCAGAAGCAG GAGGAGCAGA GGCAGCACCT GCACCTCATG GTACAGCTGC
401 TGAGGCCGCA GGATGACATC CGCCTGGCAG CCCAGCTGGA GGCACCCCGG
451 CCTCCCCGGC TCCGCTACCT GCTGGTAGTT TCTACACGAG AAGGAGAAGG
501 TCTGAGCCAG GATGAGACGG TCCTCCTGGG CGTGGATTTC CCTGACAGCA
551 GCTCCCCCAG CTGCACCCTG GGCCTGGTCT TGGCCCTCTG GAGTGACACC
601 CAGGTGTACT TAGATGGAGA CGGGGGCTTC AGCGTGACGT CTGGTGGGCA
651 AAGCCGGATC TTCAAGCCCA TCTCCATCCA GACCATGTGG TCCTCAGAAC
701 AGGAGCAGAT GGAGCAGGCG ATCCGTGCTG AGCTGTGGAA AGTGTGGAT
751 GTCAGTGACC TGGAGAGTGT CACTTCCAAA GAGATCCGCC AGGCTCTGGA
801 GCTGCGCCTG GGGCTCCCCC TCCAGCAGTA CCGTGACTTC ATCGACAACC
851 AGATGCTGCT GCTGGTGGCA CAGCGGGACC GAGCCTCCCG CATCTTCCCC
901 CACCTCTACC TGGGCTCAGA GTGGAACGCA GCAAACCTGG AGGAGCTGCA
951 GAGGAACAGG GTCACCCACA TCTTGAACAT GGCCCGGGAG ATTGACAAC
1001 TCTACCCTGA GCGCTTCACC TACCACAATG TGCGCCTCTG GGATGAGGAG
1051 TCGGCCCAGG TGCTGCCGCA CTGGAAGGAG ACGCACCGCT TCATTGAGGC
1101 TGCAAGAGCA CAGGGCACCC ACGTGCTGGT CCACTGCAAG ATGGGCGTCA
1151 GCCGCTCAGC GGCCACAGTG CTGGCCTATG CCATGAAGCA GTACGAATGC
1201 AGCCTGGAGC AGGCCCTGCG CCACGTGCAG GAGCTCCGGC CCATCGCCCG
1251 CCCCACCCCT GGCTTCCTGC GCCAGCTGCA GATCTACCAG GGCATCCTGA
1301 CGGCCAGAAC CTGAGGGTGG TGGGGAGGAG AAGGTTGTAG GCATGGAAGA
1351 GAGCCAGGCA GCCCCGAAAG AAGAGCCTGG GGCCACGGGG CACGTATAAA
1401 CCTCCGAGGG GTCATGAGGT CCATCAGTCT TCTGGAGCCC TCCTTGGGAG
1451 CTGGAGAGCA CCTCAGTAGA CCAGTGACAT GCCAGAGGTC TTCTCTTCCC
1501 ACGAGTCTTC ACATGAAGAG CCTCTGCAGC CCTTCCACA GCTTGCAAGG
1551 ACCAAGGGAG GCCAGCAGGT GGACAGGGGG CCTCAGCCTG CCCTGAAGTC
1601 CCGCCAGTCA GTGGTTACCC TCCAGGGCAG TGCCGTGGTG GCCAACC
1651 CCCAGGCCTT CCAGGAGCAG GAGCAGGGGC AGGGGCAGGG GCAGGGAGAG
1701 CCTTCGATTT CCTCTACGCC CAGGTTCGGG AAGGTGGTGA GACAGGCCAG
1751 CGTGCATGAC AGTGAGAGAG AGGGCGAGGC CTGAGCCCTC ACACATGCCC
1801 ACGCTCCCCT GACACTGAAG AGGATCCACA ACTCCTTGGA GAAACACCCT
1851 CACGTCTGTT GCCGCACACA TTCCTCTCAG CTCCGCCCCA TACCCGTCAC
1901 TACAGCCTCA CCTCCCACCC CTGTCACTAC GGCCCTACCT CCCACCCCTG
1951 TCACTACAGC CTCACCTCCT ACAGCCTTAA GTCCCAGGCC CATGTCTGCC
2001 TGTTCAAGGG CTCAAGACTT TCTAACTGGG ATGTGGTAGA GGGACTGAAG
2051 GTACCTTTGG GGGCAACAGC ACCCTAGTTT CATTCTCAAC TCTAGCCCTG
2101 CACACTCACC TGTGGCACGG AATGAAAACA GAGCTTCCCG TGCAAAAAGG
2151 GTCACGCCTC CCACCCCGC CCCCTCCCTG CACCTCCTGT CCTCTCCAG
2201 TTCAATCCTG GAACCAGCCA GGCCAGGCAA CCAGTGGCCC CCAAAGGCAG
2251 GCAGGATCCT CAGGCCCCAG CCGCGGGAGG CTGGAAGGGC TGGCAGATCG
2301 CTTCCTCAT CCACCTCCAC CGGTCCAGGT CTTTGCTGCT GTCCCCAGAC
2351 CTTCTGTGAC ACCACGCCAG ATCACAGGGC ACCAGGCCAG AGATAGTCTT
2401 CTTTGTGTCC TTTCTGGCCT CTGGCTAGTC AGTTTTTCAT AGCCTTACAG
2451 TATCTGGCTT TGTACTGAGA AATAAAACAC ATTTTCATAT TTGGTTAAAA
2501 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

FEATURES:

5' UTR: 1-88
Start: 88
Stop: 1311
3' UTR: 1315-2540

Homologous proteins:**Top 10 BLAST Hits**

	Score	E
SPLICE FORM 1:		
gi 8923483 ref NP_060327.1 hypothetical protein FLJ20515 >gi 7...	576	e-163
gi 6714641 dbj BAA89534.1 (AB036834) MAP kinase phosphatase [D...	337	2e-91
gi 8922777 ref NP_060746.1 hypothetical protein FLJ10928 >gi 7...	233	3e-60
gi 7242951 dbj BAA92536.1 (AB037719) KIAA1298 protein [Homo sa...	143	4e-33
gi 7301242 gb AAF56372.1 (AE003750) CG6238 gene product [Droso...	124	2e-27
gi 4150963 emb CAA77232.1 (Y18620) DsPTP1 protein [Arabidopsis...	113	5e-24
gi 9294518 dbj BAB02780.1 (AB023036) dual-specificity protein ...	113	5e-24
gi 6862915 gb AAF30304.1 AC018907_4 (AC018907) putative dual-sp...	94	2e-18
gi 6015037 sp O54838 DUS5_RAT DUAL SPECIFICITY PROTEIN PHOSPHAT...	92	9e-18
gi 9910432 ref NP_064570.1 mitogen-activated protein kinase ph...	90	3e-17

SPLICE FORM 2:

gi 8923483 ref NP_060327.1 hypothetical protein FLJ20515 [Homo...	576	e-163
gi 6714641 dbj BAA89534.1 (AB036834) MAP kinase phosphatase [D...	340	6e-92
gi 8922777 ref NP_060746.1 hypothetical protein FLJ10928 [Homo...	229	1e-58
gi 7242951 dbj BAA92536.1 (AB037719) KIAA1298 protein [Homo sa...	162	1e-38
gi 9294518 dbj BAB02780.1 (AB023036) dual-specificity protein ...	113	8e-24
gi 4150963 emb CAA77232.1 (Y18620) DsPTP1 protein [Arabidopsis...	113	8e-24
gi 4758212 ref NP_004411.1 dual specificity phosphatase 8 [Hom...	99	3e-19
gi 6679156 ref NP_032774.1 neuronal tyrosine/threonine phospho...	96	2e-18
gi 6862915 gb AAF30304.1 AC018907_4 (AC018907) putative dual-sp...	94	6e-18
gi 6015037 sp O54838 DUS5_RAT DUAL SPECIFICITY PROTEIN PHOSPHAT...	92	2e-17

SPLICE FORM 3:

gi 8923483 ref NP_060327.1 hypothetical protein FLJ20515 [Homo...	410	e-113
gi 8922777 ref NP_060746.1 hypothetical protein FLJ10928 [Homo...	233	7e-60
gi 6714641 dbj BAA89534.1 (AB036834) MAP kinase phosphatase [D...	224	5e-57
gi 7242951 dbj BAA92536.1 (AB037719) KIAA1298 protein [Homo sa...	143	5e-33
gi 9294518 dbj BAB02780.1 (AB023036) dual-specificity protein ...	113	1e-23
gi 4150963 emb CAA77232.1 (Y18620) DsPTP1 protein [Arabidopsis...	113	1e-23
gi 6862915 gb AAF30304.1 AC018907_4 (AC018907) putative dual-sp...	94	5e-18
gi 6015037 sp O54838 DUS5_RAT DUAL SPECIFICITY PROTEIN PHOSPHAT...	92	2e-17
gi 9910432 ref NP_064570.1 mitogen-activated protein kinase ph...	90	7e-17
gi 9911130 gb AAA64693.2 (U15932) protein phosphatase [Homo sa...	90	1e-16

BLAST to dbEST:**SPLICE FORM 1:**

	Score	E
gi 9807071 /dataset=dbest /taxon=960...	1404	0.0
gi 10317998 /dataset=dbest /taxon=96...	1316	0.0
gi 10151079 /dataset=dbest /taxon=96...	1249	0.0
gi 10401153 /dataset=dbest /taxon=960...	1180	0.0
gi 10329921 /dataset=dbest /taxon=96...	1124	0.0
gi 7632969 /dataset=dbest /taxon=960...	791	0.0
gi 9155111 /dataset=dbest /taxon=9606...	779	0.0
gi 10994242 /dataset=dbest /taxon=96...	450	e-124

EXPRESSION INFORMATION FOR MODULATORY USE:

SPLICE FORM 1:

library source:

Expression information from BLAST dbEST hits:

gi 9807071	Human Pancreas
gi 10317998	Human colon adenocarcinoma
gi 10151079	Human Pancreas:adenocarcinoma
gi 10401153	Human Pancreas:epithelioid carcinoma
gi 10329921	Human lung: large cell carcinoma
gi 7632969	Human kidney: renal cell carcinoma
gi 9155111	Human Placenta choriocarcinoma
gi 10994242	Human ovary tumor tissue

Expression information from PCR-based tissue screening panels:

Human Brain
Human Fetal brain
Human fetal heart
Human fetal kidney
Human heart
Human kidney
Human uterus
Human thyroid

SPLICE FORM 1:

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1 MALVTVSRSP PGSGASTPVG PWDQAVQRRS RLQRRQSFV LRGAVLGLQD
51 GGDNDAAEA SSEPTKAPS EEELHGDQTD FGQGSQSPQK QEEQRQHLHL
101 MVQLLRPQDD IRLAAQLEAP RPPRLRYLLV VSTREGEGLS QDETVLLGVD
151 FPDSSSPSCT LGLVLPLWSD TQVYLDGDGG FSVTSGGQSR IFKPISIQTM
201 WATLQVLHQA CEALGSGLV PGGSALTWAS HYQERLNSEQ SCLNEWTAMA
251 DLESLRPPSA EPGGSSEQEQ MEQAIRAEW KVLVDSDLES VTSKEIRQAL
301 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL
351 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE
401 AARQGTHTVL VHCKMGVSR S AATVLAYAMK QYECSEAL RHVQELRPIA
451 RPNPGFLRQL QIYQGILTAR T

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(SEE ID NO. 4)

SPLICE FORM 2:

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1 MALVTVSRSP PGSGASTPVG PWDQAVQRRS RLQRRQSFV LRGAVLGLQD
51 GGDNDAAEA SSEPTKAPS EEELHGDQTD FGQGSQSPQK QEEQRQHLHL
101 MVQLLRPQDD IRLAAQLEAP RPPRLRYLLV VSTREGEGLS QDETVLLGVD
151 FPDSSSPSCT LGLVLPLWSD TQVYLDGDGG FSVTSGGQSR IFKPISIQTM
201 WATLQVLHQA CEALGSGLV PGGSALTWAS HYQERLNSEQ SCLNEWTAMA
251 DLESLRPPSA EPGGSSEQEQ MEQAIRAEW KVLVDSDLES VTSKEIRQAL
301 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL
351 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE
401 AARQGTHTVL VHCKMGVSR S AATVLAYAMK QYECSEAL RHVQELRPIA
451 RPNPGFLRQL QIYQGILTAS RQSHVWEQKV GGVSPPEHPA PEVSTPFPLL
501 PPEPEGGGEE KVVGMEESSA APKEEPPGRP RINLRGVMRS ISLEPSLEL
551 ESTSETSDMP EVFSSHESSH EEPLQPPFQL ARTKGGQQVD RGPQPALKSR
601 QSVVTLQGSA VVANRTQAFQ EQEQQGQGQ GEPCISSTPR FRKVVRQASV
651 HDSGEEGEA

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(SEE ID NO. 5)

SPLICE FORM 3:

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1 MALVTVSRSP PGSGASTPVG PWDQAVQRRS RLQRRQSFV LRGAVLGLQD
51 GGDNDAAEA SSEPTKAPS EEELHGDQTD FGQGSQSPQK QEEQRQHLHL
101 MVQLLRPQDD IRLAAQLEAP RPPRLRYLLV VSTREGEGLS QDETVLLGVD
151 FPDSSSPSCT LGLVLPLWSD TQVYLDGDGG FSVTSGGQSR IFKPISIQTM
201 WSSEQEQQEQ AIRAELWKVL DVSDLESVTS KEIRQAELR LGLPLQQYRD
251 FIDNQMLLLV AQRDRASRIF PHLYLGSEWN AANLEELQRN RVTHILNMAR
301 EIDNFYPERF TYHNVRLWDE ESAQLLPHWK ETHRFIEAAR AQGTHVLVHC
351 KMGVSRSAAT VLAYAMKQYE CSLEQALRHV QELRPIARN PGFLRQLQIY
401 QGILTART

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(SEE ID NO. 6)

FEATURES:

Functional domains and key regions:

SPLICE FORM 1:

[1] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

34-37 RRQS

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 6

1	65-67	TEK
2	132-134	STR
3	254-256	SLR
4	292-294	TSK
5	395-397	THR
6	468-470	TAR

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 6

1	70-73	SEEE
2	132-135	STRE
3	140-143	SQDE
4	266-269	SEQE
5	286-289	SDLE
6	292-295	TSKE

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

363-369 REIDNFY

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 8

1	12-17	GSGAST
2	43-48	GAVLGL
3	47-52	GLQDGG
4	218-223	GLVPGG
5	223-228	GSALTW
6	339-344	GSEWNA
7	416-421	GVSRSA
8	465-470	GILTAR

BLAST Alignment to Top Hit:

SPLICE FORM 1:

>gi|8923483|ref|NP_060327.1| hypothetical protein FLJ20515
 >gi|7020674|dbj|BAA91228.1| (AK000522) unnamed protein
 product [Homo sapiens]
 Length = 394

Score = 576 bits (1469), Expect = e-163
 Identities = 290/312 (92%), Positives = 296/312 (93%), Gaps = 1/312 (0%)

Query: 1 MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEA 60
 MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEA
 Sbjct: 1 MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEA 60

Query: 61 SSEPTEKAPSEEEELHGDQTDGFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAP 120
 SSEPTEKAPSEEEELHGDQTDGFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAP
 Sbjct: 61 SSEPTEKAPSEEEELHGDQTDGFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAP 120

Query: 121 RPPRLRYLLVVSTREGEGLSQDETVLLGVDFPDSSSPSCTLGLVLPWSDTQVYLDGDGG 180
 RPPRLRYLLVVSTREGEGLSQDETVLLGVDFPDSSSPSCTLGLVLPWSDTQVYLDGDGG
 Sbjct: 121 RPPRLRYLLVVSTREGEGLSQDETVLLGVDFPDSSSPSCTLGLVLPWSDTQVYLDGDGG 180

Query: 181 FSVTSGGQSRIKFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASHYQERLNSEQ 240
 FSVTSGGQSRIKFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASHYQERLNSEQ
 Sbjct: 181 FSVTSGGQSRIKFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASHYQERLNSEQ 240

Query: 241 SCLNEWTAMADLESIRPPSAEPGGSSEQEQQEQAIRAELWKVLDV-SDLESVTSKEIRQA 299
 SCLNEWTAMADLESIRPPSAEPGGSSEQEQQEQAIRAELWKVL++ S E+ E+ +
 Sbjct: 241 SCLNEWTAMADLESIRPPSAEPGGSSEQEQQEQAIRAELWKVLELESTSETSDMPEVFSS 300

Query: 300 LELRLGLPLQQY 311
 E PLQ +
 Sbjct: 301 HESSHEEPLQPF 312

>gi|6714641|dbj|BAA89534.1| (AB036834) MAP kinase phosphatase
 [Drosophila melanogaster]
 Length = 1045

Score = 337 bits (854), Expect = 2e-91
 Identities = 204/537 (37%), Positives = 284/537 (51%), Gaps = 81/537 (15%)

Query: 1 MALVTVSRSPPGSGA-STPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAE 59
 MALVTV RSP +G+ S G + R + F +G L L
 Sbjct: 1 MALVTVQRSPSVAGSCSNSDGESEDDGNSKGNDRSECFAGKGTALVL----- 49

Query: 60 ASSEPTEKAPSEEEELHGDQTDGFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEA 119
 A + SE L D T +QS + + HL M LL+ +D +++A +LE+
 Sbjct: 50 ALKDIPPLTQSERRLSTDSTRSSNSTQS--NNSDIQLHLQSMFYLLQREDTLKMAVKLES 107

Query: 120 PRPPRLRYLLV-----VSTREGEGLSQDETVLLGVDFPDSSSPS----- 158
 R R RYL++ S R + + +V +G SS S
 Sbjct: 108 QRSNRTRYLVIASRSCCRSGTSDRRRHRIMRHHSVKVGGSGAGTKSSTSPAVPTQRQLSVE 167

Query: 159 -----CTLGL-----VLPLWSDTQVY 174
 C LG+ V+P+ +DT ++
 Sbjct: 168 QTATEASSKCDKTADKENATAAGDNKNTSGMEESCLLGIDCNERTTIGLVVPILADTTIH 227

Query: 175 LDGDGGFSVTSGGQSRIKFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASHYQE 234
 LDGDGGFSV ++ IFKP+S+Q MW+ LQ LH+ + A + G + W S Y+
 Sbjct: 228 LDGDGGFSVKVYEKTHIFKPVSVQAMWSALQTLHKVSKKARENNFYASGPSHDWLSSYER 287

Query: 235 RLNSEQSCLENEWAMADLES LRPPSAEP--GGSSSEQMEQAIRAELWKVLDVSDLESVT 292
R+ S+QSCLENEW AM LES RPPS + E+E+ E I+ +L ++ DL+ VT
Sbjct: 288 RIESDQSCLENEWAMDALESRRPPSPDAIRNKPPKEETESVIKMKLKAIMMSVDLDEV 347

Query: 293 SKEIRQALELRLGLPLQQYRDFIDNQMLLLVAQRDRASRIFPHLYLGSEWNAANLEELQR 352
SK IR LE L + L +Y+ FID +ML+++ Q D ++IF H+YLGSEWNA+NLEELQ+
Sbjct: 348 SKYIRGRLEEILDMDLGEYKSFIDAEMLVILGQMDAPTKIFEHVLYLGSEWNASNLEELQK 407

Query: 353 NRVTHILNMAREIDNFYPERFTYHNVRWLWDEESAQLLPHWKETHRFIEAARAQGTHVLVH 412
N V HILN+ REIDNF+P F Y NVR++D+E LL +W +T R+I A+A+G+ VLVH
Sbjct: 408 NGVRHILNVTREIDNFFPGTFEYFNVRVYDDEKTNLLKYWDDTFRYITRAKAEGSKVLVH 467

Query: 413 CKMGVSRSAATVLAYAMKQYECSEALRHVQELRPIARPNGFLRQLQIYQGILTA 469
CKMGVSRSA+ V+AYAMK Y+ +QAL HV++ R +PN FL QL+ Y G+L A
Sbjct: 468 CKMGVSRASVVIAYAMKAYQWFEQQALEHVKKRRSCIKPNKNFLNQLLETYSGLDA 524

>gi|8922777|ref|NP_060746.1| hypothetical protein FLJ10928
>gi|7023283|dbj|BAA91913.1| (AK001790) unnamed protein
product [Homo sapiens]
Length = 141

Score = 233 bits (588), Expect = 3e-60
Identities = 111/111 (100%), Positives = 111/111 (100%)

Query: 361 MAREIDNFYPERFTYHNVRWLWDEESAQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRS 420
MAREIDNFYPERFTYHNVRWLWDEESAQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRS
Sbjct: 31 MAREIDNFYPERFTYHNVRWLWDEESAQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRS 90

Query: 421 AATVLAYAMKQYECSEALRHVQELRPIARPNGFLRQLQIYQGILTART 471
AATVLAYAMKQYECSEALRHVQELRPIARPNGFLRQLQIYQGILTART
Sbjct: 91 AATVLAYAMKQYECSEALRHVQELRPIARPNGFLRQLQIYQGILTART 141

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1  CGTCCTTCCT GGTCTGCGG GTCCAGGACT GTCCGCGGGG TTGAGGGAAG
51  GGGCCGTGCC CCGTGCCAGC CCAGGTGCTC GCGGCCTGGC TCCATGGCCC
101 TGGTCACAGT GAGCCGTTTCG CCCCCGGGCA GCGGCGCCTC CACGCCCGTG
151 GGGCCCTGGG ACCAGGCGGT CCAGCGAAGG AGTCGACTCC AGCGAAGGCA
201 GAGCTTTGCG GTGCTCCGTG GGGCTGTCTT GGGACTGCAG GATGGAGGGG
251 ACAATGATGA TGCAGCAGAG GCCAGTTCTG AGCCAACAGA GAAGGCCCCG
301 AGTGAGGAGG AGCTCCACGG GGACCAGACA GACTTCGGGC AAGGATCCCA
351 GAGTCCCCAG AAGCAGGAGG AGCAGAGGCA GCACCTGCAC CTCATGGTAC
401 AGCTGCTGAG GCCGCAGGAT GACATCCGCC TGGCAGCCCA GCTGGAGGCA
451 CCCCCGCCCT CCGGCTCCG CTACCTGCTG GTAGTTTCTA CACGAGAAGG
501 AGAAGGTCTG AGCAGGATG AGACGGTCCT CCTGGGCGTG GATTTCCTTG
551 ACAGCAGCTC CCCCAGCTGC ACCCTGGGCC TGGTCTTGCC CCTCTGGAGT
601 GACACCCAGG TGTACTTAGA TGGAGACGGG GGCTTCAGCG TGACGTCTGG
651 TGGGCAAAGC CGGATCTTCA AGCCCATCTC CATCCAGACC ATGTGGGCCA
701 CACTCCAGGT ATTGCACCAA GCATGTGAGG CAGCTCTAGG CAGCGGCCTT
751 GTACCGGGTG GCAGTGCCCT CACCTGGGCC AGCCACTACC AGGAGAGACT
801 GAACTCCGAA CAGAGCTGCC TCAATGAGTG GACGGCTATG GCCGACCTGG
851 AGTCTCTGCG GCCTCCAGC GCCGAGCCTG GCGGGTCCTC AGAACAGGAG
901 CAGATGGAGC AGGCGATCCG TGCTGAGCTG TGGAAAGTGT TGGATGTCAG
951 TGACCTGGAG AGTGTCACTT CCAAAGAGAT CCGCCAGGCT CTGGAGCTGC
1001 GCCTGGGGCT CCCCCTCCAG CAGTACCGTG ACTTCATCGA CAACCAGATG
1051 CTGCTGCTGG TGGCACAGCG GGACCAGGCC TCCCGCATCT TCCCCACCT
1101 CTACCTGGGC TCAGAGTGA ACGCAGCAAA CCTGGAGGAG CTGCAGAGGA
1151 ACAGGCTCAC CCACATCTTG AACATGGCCC GGGAGATTGA CAACTTCTAC
1201 CCTGAGCGCT TCACCTACCA CAATGTGCGC CTCTGGGATG AGGAGTCGGC
1251 CCAGCTGCTG CCGCACTGGA AGGAGACGCA CCGCTTCATT GAGGCTGCAA
1301 GAGCACAGGG CACCCACGTG CTGGTCCACT GCAAGATGGG CGTCAGCCGC
1351 TCAGCGGCCA CAGTGCTGGC CTATGCCATG AAGCAGTACG AATGCAGCCT
1401 GGAGCAGGCC CTGCGCCACG TGCAGGAGCT CCGGCCATC GCCCGCCCCA
1451 ACCCTGGCTT CCTGCGCCAG CTGCAGATCT ACCAGGGCAT CCTGACGGCC
1501 AGAACCTGAG CCGTGGTGGG AGGAGAAGGT TGTAGGCATG GAAGAGAGCC
1551 AGGCAGCCCC GAAAGAAGAG CCTGGGCCAC GGCCACGTAT AAACCTCCGA
1601 GGGGTATGAG GGTCCATCAG TCTTCTGGAG CCCTCCTTGG AGCTGGAGAG
1651 CACCTCAGAG ACCAGTGACA TGCCAGAGGT CTTCTCTTCC CACGAGTCTT
1701 CACATGAAGA GCCTCTGCAG CCCTTCCCAC AGCTTGCAAG GACCAAGGGA
1751 GGCCAGCAGG TGGACAGGGG GCCTCAGCCT GCCCTGAAGT CCCGCCAGTC
1801 AGTGGTTACC CTCCAGGGCA GTGCCGTGGT GGCCAACCGG ACCCAGGCCT
1851 TCCAGGAGCA GGAGCAGGGG CAGGGGCAGG GGCAGGGAGA GCCCTGCATT
1901 TCCTCTACGC CCAGGTTCCG GAAGGTGGTG AGACAGGCCA GCGTGCATGA
1951 CAGTGGAGAG GAGGGCGAGG CCTGAGCCCT CACACATGCC CACGCTCCCC
2001 TGACACTGAA GAGGATCCAC AACTCCTTGG AGAAACACCC TCACGTCTGT
2051 TGCCGCACAC ATTCTCTCA GCTCCGCCCC ATACCCGTCA CTACAGCCTC
2101 ACCTCCCACC CCTGTCACTA CGGCCTCACC TCCCACCCCT GTCACTACAG
2151 CCTCACCTCC TACAGCCTTA AGTCCCAGGC CCATGTCTGC CTGTCCAAGG
2201 GCTCAAGACT TTCTAACTGG GATGTGGTAG AGGGACTGAA GGTACCTTTG
2251 GGGGCAACAG CACCCTAGTT TCATTCTCAA CTCTAGCCCT GCACACTCAC
2301 CTGTGGCAGC GAATGAAAAC AGAGCTTCCC GTGCAAAAAG GGTACAGCCT
2351 CCCACCCCGC CCCCCTCCCT GCACCTCCTG TCCTCTCCCA GTTCATTCTT
2401 GGAACCAGCC AGGCCAGGCA ACCAGTGGCC CCCAAAGGCA GGCAGGATCC
2451 TCAGGCCCCA GCGCGGGAG GCTGGAAGGG CTGGCAGATC GCTTCCCTCA
2501 TCCACCTCCA CCGGTCCAGG TCTTTGCTGC TGTCCCCAGA CCTCCTGTGA
2551 CACCACGCCA GATCACAGGG CACCAGGCCA GAGATAGTCT TCTTTTTGTC
2601 CTTTCTGGCC TCTGGCTAGT CAGTTTTTCA TAGCCTTACA GTATCTGGCT
2651 TTGTACTGAG AAATAAAACA CATTTTCATA AAAAAAAAAA AAAAAAAAAA
2701 AAAA

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FEATURES:

Start: 94
Exon: 94-1506
Stop: 1507

CHROMOSOME MAP POSITION:
Bac accession number: AP001885
Chromosome #: 11

ALLELIC VARIANTS (SNPs):

DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
577	G	A	Exon	162	G	S
1451	G	A	Exon	453	S	N
2641	G	A	Beyond ORF (3')			

Context:

DNA

Position

577 TCTGAGCCAACAGAGAAGGCCCGAGTGAGGAGGAGCTCCACGGGGACCAGACAGACTTC
GGGCAAGGATCCCAGAGTCCCAGAAGCAGGAGGAGCAGAGGCAGCACCTGCACCTCATG
GTACAGCTGCTGAGGCCGAGGATGACATCCGCCTGGCAGCCAGCTGGAGGCACCCCGG
CCTCCCCGGCTCCGCTACCTGCTGGTAGTTTCTACACGAGAAGGAGAAGGTCTGAGCCAG
GATGAGACGGTCTCCTGGGCGTGGATTTCCCTGACAGCAGCTCCCCAGCTGCACCTG
[G,A]
GCCTGGTCTTGCCCTCTGGAGTGACACCCAGGTGTACTTAGATGGAGACGGGGGCTTCA
GCGTGACGTCTGGTGGGCAAAGCCGGATCTTCAAGCCCATCTCCATCCAGACCATGTGGG
CCACACTCCAGGTATTGCACCAAGCATGTGAGGCAGCTCTAGGCAGCGGCCTTGTACCGG
GTGGCAGTGCCCTCACCTGGGCCAGCCACTACCAGGAGAGACTGAACTCCGAACAGAGCT
GCCTCAATGAGTGGACGGCTATGGCCGACCTGGAGTCTCTGCGGCCTCCAGCGCCGAGC

1451 ACAGGGTCACCCACATCTTGAACATGGCCCCGGGAGATTGACAACTTCTACCCTGAGCGCT
TCACCTACCACAATGTGCGCCTCTGGGATGAGGAGTCGGCCCAGCTGCTGCCGCACTGGA
AGGAGACGCACCGCTTCAATTGAGGCTGCAAGAGCACAGGGCACCACGTGCTGGTCCACT
GCAAGATGGGCGTCAGCCGCTCAGCGGCCACAGTGCTGGCCTATGCCATGAAGCAGTACG
AATGCAGCCTGGAGCAGGCCCTGCGCCACGTGCAGGAGCTCCGCCCCATCGCCCGCCCCA
[G,A]
CCCTGGCTTCTGCGCCAGCTGCAGATCTACCAGGGCATCCTGACGGCCAGAACCTGAGG
GTGGTGGGGAGGAGAAGGTTGTAGGCATGGAAGAGAGCCAGGCAGCCCCGAAAGAAGAGC
CTGGGCCACGGCCACGTATAAACCTCCGAGGGGTATGAGGTCCATCAGTCTTCTGGAGC
CCTCCTTGAGCTGGAGAGCACCTCAGAGACCAGTGACATGCCAGAGGTCTTCTCTTCCC
ACGAGTCTTCACATGAAGAGCCTCTGCAGCCCTTCCCACAGCTTGCAAGGACCAAGGGAG

2641 GGTCACGCCTCCACCCCCGCCCCCTCCCTGCACCTCCTGTCTCTCCAGTTCATTCT
GGAACCAAGCCAGGCCAGGCAACCAGTGGCCCCCAAAGGCAGGCAGGATCCTCAGGCCCA
GCCGCGGGAGGCTGGAAGGGCTGGCAGATCGCTTCCCTCATCCACCTCCACCGTCCAGG
TCTTTGCTGCTGTCCCCAGACCTCCTGTGACACCACGCCAGATCACAGGGCACCAGGCCA
GAGATAGTCTTCTTTTGTCTTTCTGGCCTCTGGCTAGTCAGTTTTTCATAGCCTTACA
[G,A]
TATCTGGCTTTGTACTGAGAAATAAAACACATTTTCATAAAAAAAAAAAAAAAAAAAAAA
AAA

GENE STRUCTURE MODEL:

SPLICE FORM 2 5'-e1-e2-e3-e4-e5-e6-e7-e8-e9-e10-e11-e12-e13-e14-3'
SPLICE FORM 1 5'-e1-e2-e3-e4-e5-e6-e7-e8-e9-e10-e11-e12-----3'
SPLICE FORM 3 5'-e1-e2-e3-e4-e5-e6----e8-e9-e10-e11-e12-----3'

MULTIPLE ALIGNMENT OF CDNA SEQUENCES:

SPLICE FORM 2 ~~~~~~TG GTTGAGGGAA
SPLICE FORM 1 CGTCCTTCCT GGTCTGCGG GTCCAGGACT GT.CCGCGGG GTTGAGGGAA
SPLICE FORM 3 ~~~~~~CCT GGTCTGCGG GTCCAGGACT GTCCCGCGG GTTGAGGGAA

51 100
SPLICE FORM 2 GGGGCCGTGC CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC

SPLICE	FORM	1	GGGGCCGTGC	CCGGTGCCAG	CCCAGGTGCT	CGCGGCCTGG	CTCCATGGCC
SPLICE	FORM	3	GGGGCCGTGC	CCGGTGCCAG	CCCAGGTGCT	CGCGGCCTGG	CTCCATGGCC
			101				150
SPLICE	FORM	2	CTGGTCACAG	TGAGCCGTTT	GCCCCCGGGC	AGCGGCGCCT	CCACGCCCGT
SPLICE	FORM	1	CTGGTCACAG	TGAGCCGTTT	GCCCCCGGGC	AGCGGCGCCT	CCACGCCCGT
SPLICE	FORM	3	CTGGTCACAG	TGAGCCGTTT	GCCCCCGGGC	AGCGGCGCCT	CCACGCCCGT
			151				200
SPLICE	FORM	2	GGGGCCCTGG	GACCAGGCGG	TCCAGCGAAG	GAGTCGACTC	CAGCGAAGGC
SPLICE	FORM	1	GGGGCCCTGG	GACCAGGCGG	TCCAGCGAAG	GAGTCGACTC	CAGCGAAGGC
SPLICE	FORM	3	GGGGCCCTGG	GACCAGGCGG	TCCAGCGAAG	GAGTCGACTC	CAGCGAAGGC
			201				250
SPLICE	FORM	2	AGAGCTTTGC	GGTGCTCCGT	GGGGCTGTCC	TGGGACTGCA	GGATGGAGGG
SPLICE	FORM	1	AGAGCTTTGC	GGTGCTCCGT	GGGGCTGTCC	TGGGACTGCA	GGATGGAGGG
SPLICE	FORM	3	AGAGCTTTGC	GGTGCTCCGT	GGGGCTGTCC	TGGGACTGCA	GGATGGAGGG
			251				300
SPLICE	FORM	2	GACAATGATG	ATGCAGCAGA	GGCCAGTTCT	GAGCCAACAG	AGAAGGCCCC
SPLICE	FORM	1	GACAATGATG	ATGCAGCAGA	GGCCAGTTCT	GAGCCAACAG	AGAAGGCCCC
SPLICE	FORM	3	GACAATGATG	ATGCAGCAGA	GGCCAGTTCT	GAGCCAACAG	AGAAGGCCCC
			301				350
SPLICE	FORM	2	GAGTGAGGAG	GAGCTCCACG	GGGACCAGAC	AGACTTCGGG	CAAGGATCCC
SPLICE	FORM	1	GAGTGAGGAG	GAGCTCCACG	GGGACCAGAC	AGACTTCGGG	CAAGGATCCC
SPLICE	FORM	3	GAGTGAGGAG	GAGCTCCACG	GGGACCAGAC	AGACTTCGGG	CAAGGATCCC
			351				400
SPLICE	FORM	2	AGAGTCCCCA	GAAGCAGGAG	GAGCAGAGGC	AGCACCTGCA	CCTCATGGTA
SPLICE	FORM	1	AGAGTCCCCA	GAAGCAGGAG	GAGCAGAGGC	AGCACCTGCA	CCTCATGGTA
SPLICE	FORM	3	AGAGTCCCCA	GAAGCAGGAG	GAGCAGAGGC	AGCACCTGCA	CCTCATGGTA
			401				450
SPLICE	FORM	2	CAGCTGCTGA	GGCCGCAGGA	TGACATCCGC	CTGGCAGCCC	AGCTGGAGGC
SPLICE	FORM	1	CAGCTGCTGA	GGCCGCAGGA	TGACATCCGC	CTGGCAGCCC	AGCTGGAGGC
SPLICE	FORM	3	CAGCTGCTGA	GGCCGCAGGA	TGACATCCGC	CTGGCAGCCC	AGCTGGAGGC
			451				500
SPLICE	FORM	2	ACCCCGGCCT	CCCCGGCTCC	GCTACCTGCT	GGTAGTTTCT	ACACGAGAAG
SPLICE	FORM	1	ACCCCGGCCT	CCCCGGCTCC	GCTACCTGCT	GGTAGTTTCT	ACACGAGAAG
SPLICE	FORM	3	ACCCCGGCCT	CCCCGGCTCC	GCTACCTGCT	GGTAGTTTCT	ACACGAGAAG
			501				550
SPLICE	FORM	2	GAGAAGGTCT	GAGCCAGGAT	GAGACGGTCC	TCCTGGGCGT	GGATTTCCCT
SPLICE	FORM	1	GAGAAGGTCT	GAGCCAGGAT	GAGACGGTCC	TCCTGGGCGT	GGATTTCCCT
SPLICE	FORM	3	GAGAAGGTCT	GAGCCAGGAT	GAGACGGTCC	TCCTGGGCGT	GGATTTCCCT
			551				600
SPLICE	FORM	2	GACAGCAGCT	CCCCCAGCTG	CACCCTGGGC	CTGGTCTTGC	CCCTCTGGAG
SPLICE	FORM	1	GACAGCAGCT	CCCCCAGCTG	CACCCTGGGC	CTGGTCTTGC	CCCTCTGGAG
SPLICE	FORM	3	GACAGCAGCT	CCCCCAGCTG	CACCCTGGGC	CTGGTCTTGC	CCCTCTGGAG
			601				650
SPLICE	FORM	2	TGACACCCAG	GTGTACTTAG	ATGGAGACGG	GGGCTTCAGC	GTGACGTCTG
SPLICE	FORM	1	TGACACCCAG	GTGTACTTAG	ATGGAGACGG	GGGCTTCAGC	GTGACGTCTG
SPLICE	FORM	3	TGACACCCAG	GTGTACTTAG	ATGGAGACGG	GGGCTTCAGC	GTGACGTCTG
			651				700
SPLICE	FORM	2	GTGGGCAAAG	CCGGATCTTC	AAGCCCATCT	CCATCCAGAC	CATGTGGGCC
SPLICE	FORM	1	GTGGGCAAAG	CCGGATCTTC	AAGCCCATCT	CCATCCAGAC	CATGTGGGCC
SPLICE	FORM	3	GTGGGCAAAG	CCGGATCTTC	AAGCCCATCT	CCATCCAGAC	CATGT....

FIGURE 3, page 3 of 8

		701				750
SPLICE	FORM 2	ACACTCCAGG	TATTGCACCA	AGCATGTGAG	GCAGCTCTAG	GCAGCGGCCT
SPLICE	FORM 1	ACACTCCAGG	TATTGCACCA	AGCATGTGAG	GCAGCTCTAG	GCAGCGGCCT
SPLICE	FORM 3
		751				800
SPLICE	FORM 2	TGTACCGGGT	GGCAGTGCCC	TCACCTGGGC	CAGCCACTAC	CAGGAGAGAC
SPLICE	FORM 1	TGTACCGGGT	GGCAGTGCCC	TCACCTGGGC	CAGCCACTAC	CAGGAGAGAC
SPLICE	FORM 3
		801				850
SPLICE	FORM 2	TGAACTCCGA	ACAGAGCTGC	CTCAATGAGT	GGACGGCTAT	GGCCGACCTG
SPLICE	FORM 1	TGAACTCCGA	ACAGAGCTGC	CTCAATGAGT	GGACGGCTAT	GGCCGACCTG
SPLICE	FORM 3
		851				900
SPLICE	FORM 2	GAGTCTCTGC	GGCCTCCCAG	CGCCGAGCCT	GGCGGGTCCT	CAGAACAGGA
SPLICE	FORM 1	GAGTCTCTGC	GGCCTCCCAG	CGCCGAGCCT	GGCGGGTCCT	CAGAACAGGA
SPLICE	FORM 3GGTCCT	CAGAACAGGA
		901				950
SPLICE	FORM 2	GCAGATGGAG	CAGGCGATCC	GTGCTGAGCT	GTGGAAAGTG	TTGGATGTCA
SPLICE	FORM 1	GCAGATGGAG	CAGGCGATCC	GTGCTGAGCT	GTGGAAAGTG	TTGGATGTCA
SPLICE	FORM 3	GCAGATGGAG	CAGGCGATCC	GTGCTGAGCT	GTGGAAAGTG	TTGGATGTCA
		951				1000
SPLICE	FORM 2	GTGACCTGGA	GAGTGTCAC	TCCAAAGAGA	TCCGCCAGGC	TCTGGAGCTG
SPLICE	FORM 1	GTGACCTGGA	GAGTGTCAC	TCCAAAGAGA	TCCGCCAGGC	TCTGGAGCTG
SPLICE	FORM 3	GTGACCTGGA	GAGTGTCAC	TCCAAAGAGA	TCCGCCAGGC	TCTGGAGCTG
		1001				1050
SPLICE	FORM 2	CGCCTGGGGC	TCCCCCTCCA	GCAGTACCGT	GACTTCATCG	ACAACCAGAT
SPLICE	FORM 1	CGCCTGGGGC	TCCCCCTCCA	GCAGTACCGT	GACTTCATCG	ACAACCAGAT
SPLICE	FORM 3	CGCCTGGGGC	TCCCCCTCCA	GCAGTACCGT	GACTTCATCG	ACAACCAGAT
		1051				1100
SPLICE	FORM 2	GCTGCTGCTG	GTGGCACAGC	GGGACCGAGC	CTCCCGCATC	TTCCCCCACC
SPLICE	FORM 1	GCTGCTGCTG	GTGGCACAGC	GGGACCGAGC	CTCCCGCATC	TTCCCCCACC
SPLICE	FORM 3	GCTGCTGCTG	GTGGCACAGC	GGGACCGAGC	CTCCCGCATC	TTCCCCCACC
		1101				1150
SPLICE	FORM 2	TCTACCTGGG	CTCAGAGTGG	AACGCAGCAA	ACCTGGAGGA	GCTGCAGAGG
SPLICE	FORM 1	TCTACCTGGG	CTCAGAGTGG	AACGCAGCAA	ACCTGGAGGA	GCTGCAGAGG
SPLICE	FORM 3	TCTACCTGGG	CTCAGAGTGG	AACGCAGCAA	ACCTGGAGGA	GCTGCAGAGG
		1151				1200
SPLICE	FORM 2	AACAGGGTCA	CCCACATCTT	GAACATGGCC	CGGGAGATTG	ACAACTTCTA
SPLICE	FORM 1	AACAGGGTCA	CCCACATCTT	GAACATGGCC	CGGGAGATTG	ACAACTTCTA
SPLICE	FORM 3	AACAGGGTCA	CCCACATCTT	GAACATGGCC	CGGGAGATTG	ACAACTTCTA
		1201				1250
SPLICE	FORM 2	CCCTGAGCGC	TTCACCTACC	ACAATGTGCG	CCTCTGGGAT	GAGGAGTCGG
SPLICE	FORM 1	CCCTGAGCGC	TTCACCTACC	ACAATGTGCG	CCTCTGGGAT	GAGGAGTCGG
SPLICE	FORM 3	CCCTGAGCGC	TTCACCTACC	ACAATGTGCG	CCTCTGGGAT	GAGGAGTCGG
		1251				1300
SPLICE	FORM 2	CCCAGCTGCT	GCCGCACTGG	AAGGAGACGC	ACCGCTTCAT	TGAGGCTGCA
SPLICE	FORM 1	CCCAGCTGCT	GCCGCACTGG	AAGGAGACGC	ACCGCTTCAT	TGAGGCTGCA
SPLICE	FORM 3	CCCAGCTGCT	GCCGCACTGG	AAGGAGACGC	ACCGCTTCAT	TGAGGCTGCA
		1301				1350
SPLICE	FORM 2	AGAGCACAGG	GCACCCACGT	GCTGGTCCAC	TGCAAGATGG	GCGTCAGCCG
SPLICE	FORM 1	AGAGCACAGG	GCACCCACGT	GCTGGTCCAC	TGCAAGATGG	GCGTCAGCCG

FIGURE 3, page 4 of 8

SPLICE FORM 3	AGAGCACAGG	GCACCCACGT	GCTGGTCCAC	TGCAAGATGG	GCGTCAGCCG
	1351				1400
SPLICE FORM 2	CTCAGCGGCC	ACAGTGCTGG	CCTATGCCAT	GAAGCAGTAC	GAATGCAGCC
SPLICE FORM 1	CTCAGCGGCC	ACAGTGCTGG	CCTATGCCAT	GAAGCAGTAC	GAATGCAGCC
SPLICE FORM 3	CTCAGCGGCC	ACAGTGCTGG	CCTATGCCAT	GAAGCAGTAC	GAATGCAGCC
	1401				1450
SPLICE FORM 2	TGGAGCAGGC	CCTGCGCCAC	GTGCAGGAGC	TCCGGCCCAT	CGCCCGCCCC
SPLICE FORM 1	TGGAGCAGGC	CCTGCGCCAC	GTGCAGGAGC	TCCGGCCCAT	CGCCCGCCCC
SPLICE FORM 3	TGGAGCAGGC	CCTGCGCCAC	GTGCAGGAGC	TCCGGCCCAT	CGCCCGCCCC
	1451				1500
SPLICE FORM 2	AACCCTGGCT	TCCTGCGCCA	GCTGCAGATC	TACCAGGGCA	TCCTGACGGC
SPLICE FORM 1	AACCCTGGCT	TCCTGCGCCA	GCTGCAGATC	TACCAGGGCA	TCCTGACG..
SPLICE FORM 3	AACCCTGGCT	TCCTGCGCCA	GCTGCAGATC	TACCAGGGCA	TCCTGACG..
	1501				1550
SPLICE FORM 2	CAGCCGCCAG	AGCCATGTCT	GGGAGCAGAA	AGTGGGTGGG	GTCTCCCCAG
SPLICE FORM 1
SPLICE FORM 3
	1551				1600
SPLICE FORM 2	AGGAGCACCC	AGCCCCTGAA	GTCTCTACAC	CATTCCCACT	TCTTCCGCCA
SPLICE FORM 1GCCA
SPLICE FORM 3GCCA
	1601				1650
SPLICE FORM 2	GAACCTGAGG	GTGGTGGGGA	GGAGAAGGTT	GTAGGCATGG	AAGAGAGCCA
SPLICE FORM 1	GAACCTGAGG	GTGGTGGGGA	GGAGAAGGTT	GTAGGCATGG	AAGAGAGCCA
SPLICE FORM 3	GAACCTGAGG	GTGGTGGGGA	GGAGAAGGTT	GTAGGCATGG	AAGAGAGCCA
	1651				1700
SPLICE FORM 2	GGCAGCCCCG	AAAGAAGAGC	CTGGG..CCA	CGGCCACGTA	TAAACCTCCG
SPLICE FORM 1	GGCAGCCCCG	AAAGAAGAGC	CTGGG..CCA	CGGCCACGTA	TAAACCTCCG
SPLICE FORM 3	GGCAGCCCCG	AAAGAAGAGC	CTGGGGCCAC	GGGGCACGTA	TAAACCTCCG
	1701				1750
SPLICE FORM 2	AGGGGTCATG	AGGTCCATCA	GTCTTCTGGA	GCCCTCCTT.	GGAGCTGGAG
SPLICE FORM 1	AGGGGTCATG	AGGTCCATCA	GTCTTCTGGA	GCCCTCCTT.	GGAGCTGGAG
SPLICE FORM 3	AGGGGTCATG	AGGTCCATCA	GTCTTCTGGA	GCCCTCCTTG	GGAGCTGGAG
	1751				1800
SPLICE FORM 2	AGCACCTCAG	.AGACCAGTG	ACATGCCAGA	GGTCTTCTCT	TCCCACGAGT
SPLICE FORM 1	AGCACCTCAG	.AGACCAGTG	ACATGCCAGA	GGTCTTCTCT	TCCCACGAGT
SPLICE FORM 3	AGCACCTCAG	TAGACCAGTG	ACATGCCAGA	GGTCTTCTCT	TCCCACGAGT
	1801				1850
SPLICE FORM 2	CTTCACATGA	AGAGCCTCTG	CAGCCCTTCC	CACAGCTTGC	AAGGACCAAG
SPLICE FORM 1	CTTCACATGA	AGAGCCTCTG	CAGCCCTTCC	CACAGCTTGC	AAGGACCAAG
SPLICE FORM 3	CTTCACATGA	AGAGCCTCTG	CAGCCCTTCC	CACAGCTTGC	AAGGACCAAG
	1851				1900
SPLICE FORM 2	GGAGGCCAGC	AGGTGGACAG	GGGGCCTCAG	CCTGCCCTGA	AGTCCCGCCA
SPLICE FORM 1	GGAGGCCAGC	AGGTGGACAG	GGGGCCTCAG	CCTGCCCTGA	AGTCCCGCCA
SPLICE FORM 3	GGAGGCCAGC	AGGTGGACAG	GGGGCCTCAG	CCTGCCCTGA	AGTCCCGCCA
	1901				1950
SPLICE FORM 2	GTCAGTGGTT	ACCCTCCAGG	GCAGTGCCGT	GGTGGCCAAC	CGGACCCAGG
SPLICE FORM 1	GTCAGTGGTT	ACCCTCCAGG	GCAGTGCCGT	GGTGGCCAAC	CGGACCCAGG
SPLICE FORM 3	GTCAGTGGTT	ACCCTCCAGG	GCAGTGCCGT	GGTGGCCAAC	CGGACCCAGG
	1951				2000

FIGURE 3, page 5 of 8

SPLICE FORM 2 CCTTCCAGGA GCAGGAGCAG GGGCAGGGGC AGGGGCAGGG AGAGCCCTGC
 SPLICE FORM 1 CCTTCCAGGA GCAGGAGCAG GGGCAGGGGC AGGGGCAGGG AGAGCCCTGC
 SPLICE FORM 3 CCTTCCAGGA GCAGGAGCAG GGGCAGGGGC AGGGGCAGGG AGAGCCCTGC

 2001 2050
 SPLICE FORM 2 ATTTCTCTA CGCCCAGGTT CCGGAAGGTG GTGAGACAGG CCAGCGTGCA
 SPLICE FORM 1 ATTTCTCTA CGCCCAGGTT CCGGAAGGTG GTGAGACAGG CCAGCGTGCA
 SPLICE FORM 3 ATTTCTCTA CGCCCAGGTT CCGGAAGGTG GTGAGACAGG CCAGCGTGCA

 2051 2100
 SPLICE FORM 2 TGACAGTGGA GAGGAGGGCG AGGCCTGAGC CCTCACACAT GCCCAGCTC
 SPLICE FORM 1 TGACAGTGGA GAGGAGGGCG AGGCCTGAGC CCTCACACAT GCCCAGCTC
 SPLICE FORM 3 TGACAGTGGA GAGGAGGGCG AGGCCTGAGC CCTCACACAT GCCCAGCTC

 2101 2150
 SPLICE FORM 2 CCCTGACACT GAAGAGGATC CACAACCTCCT TGGAGAAACA CCCTCACGTC
 SPLICE FORM 1 CCCTGACACT GAAGAGGATC CACAACCTCCT TGGAGAAACA CCCTCACGTC
 SPLICE FORM 3 CCCTGACACT GAAGAGGATC CACAACCTCCT TGGAGAAACA CCCTCACGTC

 2151 2200
 SPLICE FORM 2 TGTTCGCGCA CACATTCCTC TCAGCTCCGC CCCATACCCG TCACTACAGC
 SPLICE FORM 1 TGTTCGCGCA CACATTCCTC TCAGCTCCGC CCCATACCCG TCACTACAGC
 SPLICE FORM 3 TGTTCGCGCA CACATTCCTC TCAGCTCCGC CCCATACCCG TCACTACAGC

 2201 2250
 SPLICE FORM 2 CTCACCTCCC ACCCCTGTCA CTACGGCCTC ACCTCCCACC CCTGTCACTA
 SPLICE FORM 1 CTCACCTCCC ACCCCTGTCA CTACGGCCTC ACCTCCCACC CCTGTCACTA
 SPLICE FORM 3 CTCACCTCCC ACCCCTGTCA CTACGGCCTC ACCTCCCACC CCTGTCACTA

 2251 2300
 SPLICE FORM 2 CAGCCTCACC TCCTACAGCC TTAAGTCCCA GGCCCATGTC TGCCTGTCCA
 SPLICE FORM 1 CAGCCTCACC TCCTACAGCC TTAAGTCCCA GGCCCATGTC TGCCTGTCCA
 SPLICE FORM 3 CAGCCTCACC TCCTACAGCC TTAAGTCCCA GGCCCATGTC TGCCTGTCCA

 2301 2350
 SPLICE FORM 2 AGGGCTCAAG ACTTTCTAAC TGGGATGTGG TAGAGGGACT GAAGGTACCT
 SPLICE FORM 1 AGGGCTCAAG ACTTTCTAAC TGGGATGTGG TAGAGGGACT GAAGGTACCT
 SPLICE FORM 3 AGGGCTCAAG ACTTTCTAAC TGGGATGTGG TAGAGGGACT GAAGGTACCT

 2351 2400
 SPLICE FORM 2 TTGGGGGCAA CAGCACCCTA GTTTCATTCT CAACTCTAGC CCTGCACACT
 SPLICE FORM 1 TTGGGGGCAA CAGCACCCTA GTTTCATTCT CAACTCTAGC CCTGCACACT
 SPLICE FORM 3 TTGGGGGCAA CAGCACCCTA GTTTCATTCT CAACTCTAGC CCTGCACACT

 2401 2450
 SPLICE FORM 2 CACCTGTGGC ACGGAATGAA AACAGAGCTT CCCGTGCAAA AAGGGTCACG
 SPLICE FORM 1 CACCTGTGGC ACGGAATGAA AACAGAGCTT CCCGTGCAAA AAGGGTCACG
 SPLICE FORM 3 CACCTGTGGC ACGGAATGAA AACAGAGCTT CCCGTGCAAA AAGGGTCACG

 2451 2500
 SPLICE FORM 2 CCTCCCACCC CCGCCCCCTC CCTGCACCTC CTGTCCTCTC CCAGTTCATT
 SPLICE FORM 1 CCTCCCACCC CCGCCCCCTC CCTGCACCTC CTGTCCTCTC CCAGTTCATT
 SPLICE FORM 3 CCTCCCACCC CCGCCCCCTC CCTGCACCTC CTGTCCTCTC CCAGTTCATT

 2501 2550
 SPLICE FORM 2 CCTGGAACCA GCCAGGCCAG GCAACCAAGT GCGCCCAAAG GCAGGCAGGA
 SPLICE FORM 1 CCTGGAACCA GCCAGGCCAG GCAACCAAGT GCGCCCAAAG GCAGGCAGGA
 SPLICE FORM 3 CCTGGAACCA GCCAGGCCAG GCAACCAAGT GCGCCCAAAG GCAGGCAGGA

 2551 2600
 SPLICE FORM 2 TCCTCAGGCC CCAGCCGCGG GAGGCTGGAA GGGCTGGCAG ATCGCTTCCC
 SPLICE FORM 1 TCCTCAGGCC CCAGCCGCGG GAGGCTGGAA GGGCTGGCAG ATCGCTTCCC
 SPLICE FORM 3 TCCTCAGGCC CCAGCCGCGG GAGGCTGGAA GGGCTGGCAG ATCGCTTCCC

FIGURE 3, page 6 of 8

		2601			2650
SPLICE	FORM 2	TCATCCACCT	CCACCGGTCC	AGGTCTTTGC	TGCTGTCCCC AGACCTCCTG
SPLICE	FORM 1	TCATCCACCT	CCACCGGTCC	AGGTCTTTGC	TGCTGTCCCC AGACCTCCTG
SPLICE	FORM 3	TCATCCACCT	CCACCGGTCC	AGGTCTTTGC	TGCTGTCCCC AGACCTCCTG
		2651			2700
SPLICE	FORM 2	TGACACCACG	CCAGATCACA	GGGCACCAGG	CCAGAGATAG TCTTCTTTT
SPLICE	FORM 1	TGACACCACG	CCAGATCACA	GGGCACCAGG	CCAGAGATAG TCTTCTTTT
SPLICE	FORM 3	TGACACCACG	CCAGATCACA	GGGCACCAGG	CCAGAGATAG TCTTCTTTT
		2701			2750
SPLICE	FORM 2	GTCCTTTCTG	GCCTCTGGCT	AGTCAGTTTT	TCATAGCCTT ACAGTATCTG
SPLICE	FORM 1	GTCCTTTCTG	GCCTCTGGCT	AGTCAGTTTT	TCATAGCCTT ACAGTATCTG
SPLICE	FORM 3	GTCCTTTCTG	GCCTCTGGCT	AGTCAGTTTT	TCATAGCCTT ACAGTATCTG
		2751			2800
SPLICE	FORM 2	GCTTTGTACT	GAGAAATAAA	ACACATTTTC	ATAAAAAAAAAA AAAAAAAAAA
SPLICE	FORM 1	GCTTTGTACT	GAGAAATAAA	ACACATTTTC	ATAAAAAAAAAA AAAAAAAAAA
SPLICE	FORM 3	GCTTTGTACT	GAGAAATAAA	ACACATTTTC	ATATTTGGTT AAAAAAAAAA
		2801			2850
SPLICE	FORM 2	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA AAAAAAAAAA
SPLICE	FORM 1	AAAAAAAA~~	~~~~~	~~~~~	~~~~~
SPLICE	FORM 3	AAAAAAAAAA	AAAAAAAAAA	AAAA~	~~~~~
		2851			2894
SPLICE	FORM 2	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA AAAA
SPLICE	FORM 1	~~~~~	~~~~~	~~~~~	~~~~~
SPLICE	FORM 3	~~~~~	~~~~~	~~~~~	~~~~~
MULTIPLE ALIGNMENT OF PEPTIDE SEQUENCES:					
SPLICE	FORM 2	MALVTVSRSP	PGSGASTPVG	PWDQAVQRRS	RLQRRQSFV LRGAVLGLQD
SPLICE	FORM 1	MALVTVSRSP	PGSGASTPVG	PWDQAVQRRS	RLQRRQSFV LRGAVLGLQD
SPLICE	FORM 3	MALVTVSRSP	PGSGASTPVG	PWDQAVQRRS	RLQRRQSFV LRGAVLGLQD
		51			100
SPLICE	FORM 2	GGDNDDAEA	SSEPTKAPS	EEELHGDQTD	FGQGSQSPQK QEEQRQHLHL
SPLICE	FORM 1	GGDNDDAEA	SSEPTKAPS	EEELHGDQTD	FGQGSQSPQK QEEQRQHLHL
SPLICE	FORM 3	GGDNDDAEA	SSEPTKAPS	EEELHGDQTD	FGQGSQSPQK QEEQRQHLHL
		101			150
SPLICE	FORM 2	MVQLLRPQDD	IRLAAQLEAP	RPPRLRYLLV	VSTREGEGLS QDET VLLGVD
SPLICE	FORM 1	MVQLLRPQDD	IRLAAQLEAP	RPPRLRYLLV	VSTREGEGLS QDET VLLGVD
SPLICE	FORM 3	MVQLLRPQDD	IRLAAQLEAP	RPPRLRYLLV	VSTREGEGLS QDET VLLGVD
		151			200
SPLICE	FORM 2	FPDSSSPSCT	LGLVLPLWSD	TQVYLDGDGG	FSVTSGGQSR IFKPISIQTM
SPLICE	FORM 1	FPDSSSPSCT	LGLVLPLWSD	TQVYLDGDGG	FSVTSGGQSR IFKPISIQTM
SPLICE	FORM 3	FPDSSSPSCT	LGLVLPLWSD	TQVYLDGDGG	FSVTSGGQSR IFKPISIQTM
		201			250
SPLICE	FORM 2	WATLQVLHQA	CEAALGSLV	PGGSALTWAS	HYQERLNSEQ SCLNEWTAMA
SPLICE	FORM 1	WATLQVLHQA	CEAALGSLV	PGGSALTWAS	HYQERLNSEQ SCLNEWTAMA
SPLICE	FORM 3	W.....
		251			300
SPLICE	FORM 2	DLESLRPPSA	EPGGSSESEQ	MEQAIRAELW	KVLDVSDLES VTSKEIRQAL
SPLICE	FORM 1	DLESLRPPSA	EPGGSSESEQ	MEQAIRAELW	KVLDVSDLES VTSKEIRQAL
SPLICE	FORM 3SSEQEQ	MEQAIRAELW	KVLDVSDLES VTSKEIRQAL
		301			350

FIGURE 3, page 7 of 8

SPLICE FORM 2 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL
 SPLICE FORM 1 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL
 SPLICE FORM 3 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL

351 400

SPLICE FORM 2 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE
 SPLICE FORM 1 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE
 SPLICE FORM 3 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE

401 450

SPLICE FORM 2 AARAQGTHVL VHCKMGVSRS AATVLAYAMK QECSLEQAL RHVQELRPIA
 SPLICE FORM 1 AARAQGTHVL VHCKMGVSRS AATVLAYAMK QECSLEQAL RHVQELRPIA
 SPLICE FORM 3 AARAQGTHVL VHCKMGVSRS AATVLAYAMK QECSLEQAL RHVQELRPIA

451 500

SPLICE FORM 2 RPNPGFLRQL QIYQGILTAS RQSHVWEQKV GGVSPEEHPA PEVSTPFPLL
 SPLICE FORM 1 RPNPGFLRQL QIYQGILTAR T~~~~~
 SPLICE FORM 3 RPNPGFLRQL QIYQGILTAR T~~~~~

501 550

SPLICE FORM 2 PPEPEGGEE KVVGMEESSA APKEEPGPRP RINLRGVMRS ISLLEPSLEL
 SPLICE FORM 1 ~~~~~~
 SPLICE FORM 3 ~~~~~~

551 600

SPLICE FORM 2 ESTSETSDMP EVFSSHESSH EEPLQFPFQL ARTKGGQQVD RGPQALKSR
 SPLICE FORM 1 ~~~~~~
 SPLICE FORM 3 ~~~~~~

601 650

SPLICE FORM 2 QSVVTLQGS VVANRTQAFQ EQEQGQGQGO GEPCISSTPR FRKVVRQASV
 SPLICE FORM 1 ~~~~~~
 SPLICE FORM 3 ~~~~~~

651

SPLICE FORM 2 HDSGEEGEA
 SPLICE FORM 1 ~~~~~~
 SPLICE FORM 3 ~~~~~~

FOOTNOTES